
MAQRLEH (TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Dec 23 10:08:31 1999; MasPar time 4.19 Seconds
78.109 Million cell updates/sec

Tabular output not generated.

Title: >US-09-177-843-1
Description: (1-6) from US09177843.pep
Perfect Score: 41
Sequence: 1 GRGDSP 6

Scoring table: PAM 150
Gap 15

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sprenb19

1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human
5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle
9:sp-phase 10:sp-plant 11:sp-rodent 12:sp-unclassified
13:sp-vertebrate 14:sp-virus

Statistics: Mean 18.281; Variance 16.870; scale 1.084

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	41	100.0	1095	4	099458	2.18e+00
2	41	100.0	2478	13	093406	2.18e+00
3	40	97.6	95	1	050799	4.11e+00
4	40	97.6	347	4	099703	4.11e+00
5	40	97.6	625	11	099053	4.11e+00
6	39	95.1	1307	13	057683	7.68e+00
7	38	92.7	316	2	083343	1.42e+01
8	38	92.7	409	2	056436	1.42e+01
9	38	92.7	546	6	029111	1.42e+01
10	38	92.7	682	5	022537	1.42e+01
11	38	92.7	804	6	029113	1.42e+01
12	38	92.7	1272	13	090924	1.42e+01
13	38	92.7	1280	13	090933	1.42e+01
14	38	92.7	1369	13	042414	1.42e+01
15	37	90.2	356	7	030227	1.42e+01
16	37	90.2	511	14	091332	2.59e+01
17	37	90.2	633	2	085869	2.59e+01
18	37	90.2	1095	4	060300	2.59e+01
19	37	90.2	1190	11	097573	2.59e+01
20	37	90.2	1191	11	061181	2.59e+01

21	36	87.8	95	10	040957	4.67e+01
22	36	87.8	123	5	018672	4.67e+01
23	36	87.8	138	14	090277	4.67e+01
24	36	87.8	235	1	P71164	4.67e+01
25	36	87.8	250	11	Q61571	4.67e+01
26	36	87.8	255	11	Q61570	4.67e+01
27	36	87.8	339	5	Q18218	4.67e+01
28	36	87.8	511	2	Q24819	4.67e+01
29	36	87.8	568	2	Q44106	4.67e+01
30	36	87.8	699	10	Q64525	4.67e+01
31	36	87.8	1240	14	P89453	4.67e+01
32	36	87.8	3766	5	Q17551	4.67e+01
33	35	85.4	157	2	Q04915	8.32e+01
34	35	85.4	304	2	P96903	8.32e+01
35	35	85.4	335	11	Q08283	8.32e+01
36	35	85.4	367	3	P78852	8.32e+01
37	35	85.4	541	11	P70430	8.32e+01
38	35	85.4	551	10	Q81469	8.32e+01
39	35	85.4	763	3	Q60013	8.32e+01
40	35	85.4	802	11	P70433	8.32e+01
41	35	85.4	1068	11	Q54826	8.32e+01
42	35	85.4	1083	5	Q26423	8.32e+01
43	35	85.4	1201	5	Q18393	8.32e+01
44	35	85.4	1276	11	P97260	8.32e+01
45	35	85.4	1920	6	Q29519	8.32e+01

ALIGNMENTS

RESULT 1 PRELIMINARY; PRT: 1095 AA.
ID Q99458;
AC Q99458;
DT 01-MAY-1997 (TREMREL. 03, CREATED)
DT 01-MAY-1997 (TREMREL. 03, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMREL. 09, LAST ANNOTATION UPDATE)
DE NOTCH4 (FRAGMENT).
GN NOTCH4.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC CAVARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE; 97311416.
RA SUGAYA K., SASANUMA S., NOHATA J., KIMURA T., FUKAGAWA T.,
RA NAKAMURA Y., ANDO A., INOKO H., IKEMURA T., MITA K.;
RT "Gene organization of human NOTCH4 and (CTG)n polymorphism in this
RT human counterpart gene of mouse proto-oncogene Int3.";
RL GENE 189:235-244(1997).
DR EMBL; D63395; D1010354; -.
DR PROSITE; PS01186; EGF_2; 5.
DR PFAM; PF00008; EGF; 5.
DR PFAM; PF00023; ank; 5.
DR PFAM; PF00066; notch; 2.
KW GLYCOPROTEIN.
FT NON_TER 1 1
SQ SEQUENCE 1095 AA; 114807 MW; 598EA191 CRC32;
Query Match 100.0%; Score 41; DB 4; Length 1095;
Best Local Similarity 100.0%; Pred. No. 2.18e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 547 GRGDSP 552
QY 1 GRGDSP 6
RESULT 2 PRELIMINARY; PRT: 2478 AA.
ID Q93406;
AC Q93406;
DT 01-NOV-1998 (TREMREL. 08, CREATED)
DT 01-NOV-1998 (TREMREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMREL. 08, LAST ANNOTATION UPDATE)

DE FIBRONECTIN.
GN ZFN.
OS BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANTO).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
OC TELIOSTEI; EUTELEOSTEI; OSTARIOPHYSI; CYPRINIFORMES; CYPRINOIDEA;
OC CYPRINIDAE; RASBORINAE; DANIO.
RN [1]
RP SEQUENCE FROM N.A.
RA ZHAO Q., COLLODI P.;
RT "Characterization and expression of zebrafish fibronectin."
RL SUBMITTED (JUL-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF081128; G3420846; -;
DR PROSITE: PS00023; FIBRONECTIN_2; 2;
SQ SEQUENCE 2478 AA; 271652 MW; 1991DF70 CRC32;
Query Match 100.0%; Score 41; DB 13; Length 2478;
Best Local Similarity 100.0%; Pred. No. 2.18e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1613 GRGDSF 1618
QY 1 GRGDSF 6
|||||
RESULT 3
ID Q50799 PRELIMINARY; PRT; 95 AA.
AC Q50799;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE COBAL TRANSFER PROTEIN CBIN.
GN CBIN.
OS METHANOBACTERIUM THERMOAUTOTROPHICUM (STRAIN MARBURG).
OC ARCHAEA; EUKARYOTA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC METHANOBACTERIUM.
RN [1]
RP SEQUENCE FROM N.A.
RA EBERHARDT S., KORN S., LOTTSPEICH F., BACHER A.;
RL BACTERIOL. 179:2938-2943(1997).
CC -!- FUNCTION: MAY BE INVOLVED WITH COBAL TRANSFER IN ASSOCIATION
WITH COBALAMIN BIOSYNTHESIS.
CC -!- PATHWAY: COBALAMIN BIOSYNTHESIS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
DR EMBL: X94292; E237183; -;
KW COBALAMIN BIOSYNTHESIS; TRANSFER; COBAL TRANSFER; TRANSMEMBRANE.
FT TRANSMEM 7 27 POTENTIAL.
FT TRANSMEM 67 87 POTENTIAL.
SQ SEQUENCE 95 AA; 10254 MW; 81CE9869 CRC32;
Query Match 97.8%; Score 40; DB 1; Length 95;
Best Local Similarity 83.3%; Pred. No. 4.11e+00;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 89 GRGESP 94
QY 1 GRGDSF 6
|||||
RESULT 4
ID Q99703 PRELIMINARY; PRT; 347 AA.
AC Q99703;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE ATAXIN-2 RELATED PROTEIN (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC CATARRHINI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97051920.
RA PULST S.M., NESCHPORUK A., NECHPORUK T., GISPET S., CHEN X.N.,
RA LOPES-CENDES I., PEARLMAN S., STARKMAN S., OROZCO-DIAZ G., LUNKES A.,
RA DEJONG P., ROULEAU G.A., AUBURGER G., KORENBERG J.R., FIGUEROA C.,
RA SABA S.;
RT "Moderate expansion of a normally biallelic trinucleotide repeat in
spino cerebellar ataxia type 2.";
RL NAT. GENET. 14:269-276(1996).
DR EMBL: U70671; G1679686; -;
FT NON_TER 1 1
SQ SEQUENCE 347 AA; 37805 MW; 9BD963F2 CRC32;
Query Match 97.6%; Score 40; DB 4; Length 347;
Best Local Similarity 83.3%; Pred. No. 4.11e+00;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 283 GRGESP 288
QY 1 GRGDSF 6
|||||
RESULT 5
ID Q99053 PRELIMINARY; PRT; 625 AA.
AC Q99053;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE FILAGRIN (FRAGMENT).
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LIVER;
RX MEDLINE: 90274870.
RA HAYDOCK P.V., DALE B.A.;
RT "Filaggrin, an intermediate filament-associated protein: structural
and functional implications from the sequence of a cDNA from rat.";
RL DNA CELL BIOL. 9:251-261(1990).
CC -!- FUNCTION: FILAGRIN AGGREGATES KERATIN INTERMEDIATE FILAMENTS AND
PROMOTES DISULFIDE-BOND FORMATION AMONGST THE INTERMEDIATE
FILAMENTS DURING TERMINAL DIFFERENTIATION OF MAMMALIAN EPIDERMIS.
CC -!- FILAGRIN IS INITIALLY SYNTHESIZED AS A LARGE, INSOLUBLE, HIGHLY
PHOSPHORYLATED PRECURSOR CONTAINING MANY TANDEM COPIES OF 380 AA,
WHICH ARE SEPARATED BY "LINKERS" OF 26 AA.
CC THE PRECURSOR IS DEPOSITED AS KERATOHYALIN GRANULES.
CC DURING TERMINAL DIFFERENTIATION IT IS DEPHOSPHORYLATED &
PROTEOLYTICALLY CLEAVED.
CC -!- TISSUE SPECIFICITY: EPIDERMIS, PALATE AND FORESTOMACH.
DR EMBL: M21759; G204144; -;
DR PIR: A34615; A34615
KW DEVELOPMENTAL PROTEIN; PHOSPHORYLATION; POLYPROTEIN.
FT NON_TER 1 1
SQ SEQUENCE 625 AA; 65957 MW; 6CD02B43 CRC32;
Query Match 97.6%; Score 40; DB 11; Length 625;
Best Local Similarity 83.3%; Pred. No. 4.11e+00;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 126 GRGESP 131
QY 1 GRGDSF 6
|||||
RESULT 6
ID Q57683 PRELIMINARY; PRT; 1307 AA.
AC Q57683;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE 146KDA NUCLEAR PROTEIN.
OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
OC MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
RN [1]
RP SEQUENCE FROM N.A.

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RA SCHMIDT-ZACHMANN M.S., KNECHT S., KRAEMER A.;
RL MOL. BIOL. CELL 9:143-160(1998).
DR EMBL; Y08997; E291018; -.
KW NUCLEAR PROTEIN.
SQ SEQUENCE 1307 AA; 146213 MW; F9E016BD CRC32;

Query Match
Best Local Similarity 95.1%; Score 39; DB 13; Length 1307;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 272 GRGDP 277
   ||||:|
QY 1 GRGDSP 6

RESULT 7
ID 083343 PRELIMINARY; PRT; 316 AA.
AC 083343;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DE RIBOSE/GALACTOSE ABC TRANSPORTER, PERMEASE PROTEIN (RBSC-2).
GN TP0323.
OS TREPONEMA PALLIDUM.
OC BACTERIA; SPIROCHAETALES; SPIROCHAETACEAE; TREPONEMA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98332770.
RA FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
RA DODSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A.,
RA SODERGREN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,
RA KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T.,
RA MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S.,
RA HATCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O.,
RA VENTER J.C.;
RT "Complete Genome Sequence of Treponema pallidum, the Syphilis
RT Spirochete.";
RN SCIENCE 281:375-388(1998).
[2]
RA SEQUENCE FROM N.A.
RA FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
RA DODSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A.,
RA SODERGREN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,
RA KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T.,
RA MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S.,
RA HATCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O.,
RA VENTER J.C.;
RL SUBMITTED (MAR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AE001212; G3322600; -.
SQ SEQUENCE 316 AA; 33824 MW; CE7DB8A0 CRC32;

Query Match
Best Local Similarity 92.7%; Score 38; DB 2; Length 316;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 298 GRGEAP 303
   ||||:|
QY 1 GRGDSP 6

RESULT 8
ID Q56436 PRELIMINARY; PRT; 469 AA.
AC Q56436;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE S-LAYER-LIKE PROTEIN.
GN SLP.
OS THERMUS AQUATICUS (SUBSP. THERMOPHILUS).
OC BACTERIA; THERMUS/DEINOCOCCUS GROUP; THERMUS GROUP; THERMUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HB8;

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RA OLABARRIA G., FERNANDEZ-HERRERO L.A., CARRASCOSA J.L., BERENGUER J.;
RL J. BACTERIOL. 178:357-365(1995).
DR EMBL; X90369; G993026; -.
KW S-LAYER.
SQ SEQUENCE 469 AA; 52131 MW; 87F62633 CRC32;

Query Match
Best Local Similarity 92.7%; Score 38; DB 2; Length 469;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 178 GRGEAP 183
   ||||:|
QY 1 GRGDSP 6

RESULT 9
ID 029111 PRELIMINARY; PRT; 546 AA.
AC 029111;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE SCAVENGER-RECEPTOR PROTEIN PRECURSOR (FRAGMENT).
GN WCL.
OS SUS SCROFA (PIG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
OC ARTIODACTYLA; SUIFORMES; SUINA; SUIDAE; SUS.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-SLAB/B;
RX MEDLINE; 97364683.
RA KANAN J.H.C., NAYEM N., BINNS R.M., CHAIN B.M.;
RT "Mechanisms for variability in a member of the scavenger-receptor
RT cysteine-rich superfamily.";
RL IMMUNOGENETICS 46:276-282(1997).
DR EMBL; X99334; E254903; -.
DR PFAM; PF00530; SRCR; 5.
KW SIGNAL.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 >546 SCAVENGER-RECEPTOR PROTEIN.
FT NON_TER 546 546
SQ SEQUENCE 546 AA; 59112 MW; F98A0F1F CRC32;

Query Match
Best Local Similarity 92.7%; Score 38; DB 6; Length 546;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 83 GRGDSP 88
   ||||:|
QY 1 GRGDSP 6

RESULT 10
ID Q22537 PRELIMINARY; PRT; 682 AA.
AC Q22537;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE SIMILARITY TO COLLAGEN.
GN T1H7.1
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-BRISTOL N2;
RX MEDLINE; 94150718.
RA WILSON R., AINSOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

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RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL NATURE 368:32-38(1994).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA FAVELLO A.;
 RL SUBMITTED (JAN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: U42841; G1125784;
 SQ SEQUENCE 682 AA; 72150 MW; 0EF72EE3 CRC32;

Query Match 92.7%; Score 38; DB 5; Length 682;
 Best Local Similarity 83.3%; Pred. No. 1.42e+01;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 228 GRGDGP 233
 |||||
 QY 1 GRGDSP 6

RESULT 11
 ID Q29113 PRELIMINARY; PRT; 804 AA.
 AC Q29113;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE SCAVENGER-RECEPTOR PROTEIN PRECURSOR.
 GN WCL
 OS SUS SCROFA (PIG).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 OC ARTIODACTYLA; SUIFORMES; SUINA; SUIDAE; SUS.
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-SLAB/B;
 RX MEDLINE; 97364683.
 RA KANAN J.H.C., NAYEM N., BINNS R.M., CHAIN B.M.;
 RT "Mechanisms for variability in a member of the scavenger-receptor
 RT cysteine-rich superfamily.";
 RL IMMUNOGENETICS 46:276-282(1997).
 DR EMBL: X99336; E254904;
 DR PFAM; PF00530; SRCR; 5.
 KW SIGNAL.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 >804 SCAVENGER-RECEPTOR PROTEIN.
 SQ SEQUENCE 804 AA; 86627 MW; 64125250 CRC32;

Query Match 92.7%; Score 38; DB 6; Length 804;
 Best Local Similarity 83.3%; Pred. No. 1.42e+01;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 83 GRGDGP 88
 |||||
 QY 1 GRGDSP 6

RESULT 12
 ID Q90924 PRELIMINARY; PRT; 1272 AA.
 AC Q90924;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE NEUROFASCIN PRECURSOR.
 OS GALLUS GALLUS (CHICKEN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
 OC NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE; 92317154.
 RA VOLKMER H., HASSEL B., WOLFF J.M., FRANK R., RATHJEN F.G.;

RT "Structure of the axonal surface recognition molecule neurofascin and
 RT its relationship to a neural subgroup of the immunoglobulin
 RT superfamily.";
 RL J. CELL BIOL. 118:149-161(1992).
 DR EMBL: X65224; G63660;
 DR PFAM; PF00041; fn3; 4.
 DR PFAM; PF00047; ig; 6.
 KW SIGNAL.
 FT SIGNAL 1 25 POTENTIAL.
 SQ SEQUENCE 1272 AA; 142242 MW; 02CCB48F CRC32;

Query Match 92.7%; Score 38; DB 13; Length 1272;
 Best Local Similarity 83.3%; Pred. No. 1.42e+01;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 928 GRGDGP 933
 |||||
 QY 1 GRGDSP 6

RESULT 13
 ID Q90933 PRELIMINARY; PRT; 1280 AA.
 AC Q90933;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE NEURON-GLIA CELL ADHESION MOLECULE (NG-CAM) PRECURSOR (NG-CAM).
 OS GALLUS GALLUS (CHICKEN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
 OC NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-WHITE LEHORN; TISSUE-BRAIN;
 RX MEDLINE; 97133428.
 RA BUCHSTALLER A., KUNZ S., BERGER P., KUNZ B., ZIEGLER U., RADER C.,
 RA SONDEREGGER P.;
 RT "Cell adhesion molecules NgCAM and axonin-1 form heterodimers in the
 RT neuronal membrane and cooperate in neurite outgrowth promotion.";
 RL J. CELL BIOL. 135:1593-1607(1996).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN-WHITE LEHORN; TISSUE-BRAIN;
 RX MEDLINE; 91154306.
 RA BURGON M.P., GRUMET M., MAURO V., EDELMAN G.M., CUNNINGHAM B.A.;
 RT "Structure of the chicken neuron-glia cell adhesion molecule, Ng-CAM:
 RT origin of the polypeptides and relation to the Ig superfamily.";
 RL J. CELL BIOL. 112:1017-1029(1991).
 DR EMBL: Z75013; E256949;
 DR PFAM; PF00041; fn3; 5.
 DR PFAM; PF00047; ig; 6.
 KW SIGNAL.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 1280 NEURON-GLIA CELL ADHESION MOLECULE
 (NG-CAM).
 SQ SEQUENCE 1280 AA; 138432 MW; A72DEE34 CRC32;

Query Match 92.7%; Score 38; DB 13; Length 1280;
 Best Local Similarity 83.3%; Pred. No. 1.42e+01;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 919 GRGDGP 924
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 QY 1 GRGDSP 6

RESULT 14
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 AC O42414;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE NEUROFASCIN PRECURSOR.
 OS GALLUS GALLUS (CHICKEN).

Search completed: Thu Dec 23 10:09:11 1999
Job time : 40 secs.

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OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
OC NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA HASSEL B., RATHJEN F.G., VOLKMER H.;
RA MEDLINE; 98019255.
RT "Organization of the neurofascin gene and analysis of developmentally
RL regulated alternative splicing.";
RL J. BIOL. CHEM. 272:28742-28749(1997).
DR EMBL; Y14343; E331970; JOINED.
DR EMBL; Y14344; E331970; JOINED.
DR EMBL; Y14345; E331970; JOINED.
DR EMBL; Y14346; E331970; JOINED.
DR EMBL; Y14347; E331970; JOINED.
DR EMBL; Y14348; E331970; JOINED.
DR EMBL; Y14341; E331970; -.
DR EMBL; Y14342; E331970; JOINED.
DR EMBL; Y14349; E331970; JOINED.
DR EMBL; Y14353; E331970; JOINED.
DR EMBL; Y14354; E331970; JOINED.
DR EMBL; Y14350; E331970; JOINED.
DR EMBL; Y14351; E331970; JOINED.
DR EMBL; Y14352; E331970; JOINED.
DR PFAM; PF00041; fn3; 5.
DR PFAM; PF00047; 19; 6.
KW SIGNAL.
FT SIGNAL
FT CHAIN
SQ SEQUENCE 1369 AA; 152954 MW; F926E6B4 CRC32;

Query Match 92.7%; Score 38; DB 13; Length 1369;
Best Local Similarity 83.3%; Pred. No. 1.42e+01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 928 GRGDGP 933
Qy 1 GRGDSP 6

RESULT 15
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AC Q30227;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE MHC CLASS I AOTR-G*02 (FRAGMENT).
GN AOTR-G.
OS AOTUS TRIVIRGATUS (NIGHT MONKEY) (DOUROUCOULI).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC PLATYRRHINI; CEBIDAE; AOTINAE; AOTUS.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE; 98070787.
RA CADAVIN L.F., SHUFFLEBOTHAM C., RUIZ F.J., YEAGER M., HUGHES A.L.,
RA WATKINS D.I.;
RT "Evolutionary instability of the major histocompatibility complex
RL class I loci in New World primates.";
RL PROC. NATL. ACAD. SCI. U.S.A. 94:14536-14541(1997).
DR EMBL; U59645; G1389917; -.
DR PFAM; PF00047; 19; 1.
DR PFAM; PF00129; MHC_I; 1.
DR KW MHC.
FT NON_TER
FT SEQUENCE 356 AA; 39726 MW; B3A2E8B0 CRC32;

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Db 32 GRGEPP 37
Qy 1 GRGDSP 6

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